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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/800,198

DATE: 10/29/2001
 TIME: 15:42:22

Input Set : A:\Cura-191.app
 Output Set: N:\CRF3\10292001\I800198.raw

3 <110> APPLICANT: Vernet, Cornie AM
 4 Fernandes, Elma
 5 Shimkets, Richard A
 6 Herrmann, John L
 7 Majumder, Kumud
 8 Mishra, Vishna
 9 Mezes, Peter S
 10 Rastelli, Luca
 12 <120> TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 14 <130> FILE REFERENCE: 15966-697
 16 <140> CURRENT APPLICATION NUMBER: 09/800198
 17 <141> CURRENT FILING DATE: 2001-03-05
 19 <150> PRIOR APPLICATION NUMBER: 60/186,596
 20 <151> PRIOR FILING DATE: 2000-03-03
 22 <160> NUMBER OF SEQ ID NOS: 98
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 771
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (438)..(752)
 35 <400> SEQUENCE: 1
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 40 attggcagcc ttagaacttag tgggaaggcg ggtgcgcgaa gtcgagggggc ggagagaggg 180
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 48 tcgtgtcaca tccatatgac acttggaatg tgacaggcga ggatgtgatc tttggctgtg 420
 50 aagtgtttgc ctacccc atg gcc tcc atc gag tgg agg aag gat ggc ttg 470
 51 Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu
 52 1 5 10
 54 gac atc cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg 518
 55 Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg
 56 15 20 25
 58 ggt gga ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct 566
 59 Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala
 60 30 35 40
 62 gtg cgt ccc agt gat gag ggc act tac cgc tgc ctt gcc cgc aat gcc 614
 63 Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala
 64 45 50 55
 66 ctg ggt caa gtg gag gcc cct gct agc ttg aca gtg ctc aca cct gac 662
 67 Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp
 68 60 65 70 75
 70 cag ctg aac tct aca ggc atc ccc cag ctg cga tca cta aac ctg gtt 710

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71 Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val
72 80 85 90
74 cct gag gag gag gct gag agt gaa gag aat gac gat tac tac 752
75 Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
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78 taggtccaga gctctggcc 771
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82 <211> LENGTH: 105
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
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88 1 5 10 15
90 Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly Pro Gln Arg
91 20 25 30
93 Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg Pro Ser Asp
94 35 40 45
96 Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala Leu Gly Gln Val Glu
97 50 55 60
99 Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp Gln Leu Asn Ser Thr
100 65 70 75 80
102 Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val Pro Glu Glu Glu Ala
103 85 90 95
105 Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
106 100 105
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111 <211> LENGTH: 5502
112 <212> TYPE: DNA
113 <213> ORGANISM: Homo sapiens
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (420)..(2864)
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124 gcccggcag gtcattaaatt ccattttttt ttagagtatc acagttttct ccttcactga 180
126 ccacccttttgc ttccctgtca gaaagccctg gacagaactc tctgtggat tctgcccatt 240
128 ttcttgat atcgcccaa ttgtccctggc tgggctgtcg ggtctgcccgttttacat 300
130 gggcaaactg gagtggaaat tatccgggtg gcttcctcag gcctgcagct ggtggagcag 360
132 ctactgaaac aatcaggagc ccagaagctt tgaagtccaca agaagagaag actccccaga 419
134 atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467
135 Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys
136 1 5 10 15
138 cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515
139 Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn
140 20 25 30
142 gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563
143 Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
144 35 40 45

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146	tgc	gtg	ctc	agc	agg	aag	aca	ggg	gag	ccc	gaa	tgc	cag	tgc	ctg	gag	611
147	Cys	Val	Leu	Ser	Arg	Lys	Thr	Gly	Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu	
148	50						55					60					
150	gca	tgc	agg	ccc	agc	tac	gtg	cct	gtg	tgc	ggc	tct	gat	ggg	agg	ttt	659
151	Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe	
152	65						70					75			80		
154	tat	gaa	aac	cac	tgt	aag	ctc	cac	cgt	gct	gct	tgc	ctc	ctg	gga	aag	707
155	Tyr	Glu	Asn	His	Cys	Lys	Leu	His	Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys	
156							85					90			95		
158	agg	atc	acc	gtc	atc	cac	agc	aag	gac	tgt	ttc	ctc	aaa	ggt	gac	acg	755
159	Arg	Ile	Thr	Val	Ile	His	Ser	Lys	Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr	
160							100					105			110		
162	tgc	acc	atg	gcc	ggc	tac	gcc	cgc	ttg	aag	aat	gtc	ctt	ctg	gca	ctc	803
163	Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu	
164							115					120			125		
166	cag	acc	cgt	ctg	cag	cca	ctc	caa	gaa	gga	gac	agc	aga	caa	gac	cct	851
167	Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro	
168							130					135			140		
170	gcc	tcc	cag	aag	cgc	ctc	ctg	gtg	gaa	tct	ctg	ttc	agg	gac	tta	gat	899
171	Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp	
172	145						150					155			160		
174	gca	gat	ggc	aat	ggc	cac	ctc	agc	agc	tcc	gaa	ctg	gct	cag	cat	gtg	947
175	Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	Ser	Ser	Glu	Leu	Ala	Gln	His	Val	
176							165					170			175		
178	ctg	aag	aag	cag	gac	ctg	gat	gaa	gac	tta	ctt	ggt	tgc	tca	cca	ggt	995
179	Leu	Lys	Gln	Asp	Leu	Asp	Glu	Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly		
180							180					185			190		
182	gac	ctc	ctc	cga	ttt	gac	gat	tac	aac	agt	gac	agc	tcc	ctg	acc	ctc	1043
183	Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu	
184							195					200			205		
186	cgc	gag	ttc	tac	atg	gcc	ttc	caa	gtg	gtt	cag	ctc	agc	ctc	gcc	ccc	1091
187	Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	Val	Val	Gln	Leu	Ser	Leu	Ala	Pro	
188							210					215			220		
190	gag	gac	agg	gtc	agt	gtg	acc	aca	gtg	acc	gtg	ggg	ctg	agc	aca	gtg	1139
191	Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	Val	Thr	Val	Gly	Leu	Ser	Thr	Val	
192	225						230					235			240		
194	ctg	acc	tgc	gcc	gtc	cat	gga	gac	ctg	agg	cca	cca	atc	atc	tgg	aag	1187
195	Leu	Thr	Cys	Ala	Val	His	Gly	Asp	Leu	Arg	Pro	Pro	Ile	Ile	Trp	Lys	
196							245					250			255		
198	cgc	aac	ggg	ctc	acc	ctg	aac	ttc	ctg	gac	ttg	gaa	gac	atc	aat	gac	1235
199	Arg	Asn	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Asp	Leu	Glu	Asp	Ile	Asn	Asp	
200							260					265			270		
202	ttt	gga	gag	gat	gat	tcc	ctg	tac	atc	acc	aag	gtg	acc	acc	atc	cac	1283
203	Phe	Gly	Glu	Asp	Asp	Ser	Leu	Tyr	Ile	Thr	Lys	Val	Thr	Thr	Ile	His	
204							275					280			285		
206	atg	ggc	aat	tac	acc	tgc	cat	gct	tcc	ggc	cac	gag	cag	ctg	ttc	cag	1331
207	Met	Gly	Asn	Tyr	Thr	Cys	His	Ala	Ser	Gly	His	Glu	Gln	Leu	Phe	Gln	
208							290					295			300		
210	acc	cac	gtc	ctg	cag	gtg	aat	gtg	ccg	cca	gtc	atc	cgt	gtc	tat	cca	1379

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211	Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro				
212	305	310	315	320	
214	gag agc cag gca cag gag cct gga gtg gca gcc agc cta aga tgc cat				1427
215	Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His				
216	325	330	335		
218	gct gag ggc att ccc atg ccc aga atc act tgg ctg aaa aac ggc gtg				1475
219	Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val				
220	340	345	350		
222	gat gtc tca act cag atg tcc aaa cag ctc tcc ctt tta gcc aat ggg				1523
223	Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly				
224	355	360	365		
226	agc gaa ctc cac atc agc agt gtt cgg tat gaa gac aca ggg gca tac				1571
227	Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr				
228	370	375	380		
230	acc tgc att gcc aaa aat gaa gtc ggt gtg gat gaa gat atc tcc tcg				1619
231	Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser				
232	385	390	395	400	
234	ctc ttc att gaa gac tca gct aga aag acc ctt gca aac atc ctg tgg				1667
235	Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp				
236	405	410	415		
238	cga gag gaa ggc ctc agc gtg gga aac atg ttc tat gtc ttc tcc gac				1715
239	Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp				
240	420	425	430		
242	gac ggt atc atc gtc atc cat cct gtg gac tgt gag atc cag agg cac				1763
243	Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His				
244	435	440	445		
246	ctc aaa ccc acg gaa aag att ttc atg agc tat gaa gaa atc tgt cct				1811
247	Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro				
248	450	455	460		
250	caa aga gaa aaa aat gca acc cag ccc tgc cag tgg gta tct gca gtc				1859
251	Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val				
252	465	470	475	480	
254	aat gtc cgg aac cgg tac atc tat gtg gcc cag cca gca ctg agc aga				1907
255	Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg				
256	485	490	495		
258	gtc ctt gtg gtc gac atc caa gcc cag aaa gtc cta cag tcc ata ggt				1955
259	Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly				
260	500	505	510		
262	gtg gac cct ctg cgg gct aag ctg tcc tat gac aag tca cat gac caa				2003
263	Val Asp Pro Leu Pro Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln				
264	515	520	525		
266	gtg tgg gtc ctg agc tgg ggg gac gtg cac aag tcc cga cca agt ctc				2051
267	Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu				
268	530	535	540		
270	cag gtg atc aca gaa gcc agc acc ggc cag agc cag cac ctc atc cgc				2099
271	Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg				
272	545	550	555	560	
274	aca ccc ttt gca gga gtg gat gat ttc ttc att ccc cca aca aac ctc				2147
275	Thr Pro Phe Ala Gly Val Asp Phe Phe Ile Pro Pro Thr Asn Leu				

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276	565	570	575	
278	atc atc aac cac atc agg ttt ggc ttc atc ttc aac aag tct gat cct			2195
279	Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro			
280	580	585	590	
282	gca gtc cac aag gtg gac ctg gaa aca atg atg ccc ctc aag acc atc			2243
283	Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile			
284	595	600	605	
286	ggc ctg cac cac cat ggc tgc gtg ccc cag gcc atg gca cac acc cac			2291
287	Gly Leu His His Gly Cys Val Pro Gln Ala Met Ala His Thr His			
288	610	615	620	
290	ctg ggc ggc tac ttc atc cag tgc cga cag gac agc ccc gcc tct			2339
291	Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser			
292	625	630	635	640
294	gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc			2387
295	Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly			
296	645	650	655	
298	ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc			2435
299	Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg			
300	660	665	670	
302	ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag			2483
303	Phe Ile Val Ser Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu			
304	675	680	685	
306	atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac			2531
307	Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn			
308	690	695	700	
310	tcg ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat			2579
311	Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn			
312	705	710	715	720
314	caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc			2627
315	Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe			
316	725	730	735	
318	ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag			2675
319	Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu			
320	740	745	750	
322	cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg			2723
323	Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met			
324	755	760	765	
326	agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag			2771
327	Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu			
328	770	775	780	
330	tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg			2819
331	Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val			
332	785	790	795	800
334	tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta			2864
335	Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val			
336	805	810	815	
338	tgaaggcccc agagcagagc cctggggccaa ggaacacccc ctagtcctga cactgcagcc			2924
340	tcaagcaggt acgctgtaca ttttacaga caaaaagcaaa aacctgtact cgctttgtgg			2984
342	ttcaaacactg gtctccttgc aagtttcccta gtataaggtt tgccgtgcta ccaagattgg			3044

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